NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE-SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Tila nuclacida u	11 0.0,020 0.0,023
comply with the requirements for the following reason(s):	sequence disclosure contained in this application does not such a disclosure as set forth in 37 C.F.R. 1.321 - 1.325 for
	•

i. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.325. Applicant attention is directed to these regulations, published at 1114 CG 29, May 15, 1990 and at 55 FR. 1823C, May 1, 1990.
2. This addication does not contain, as a separate part of the disclosure on paper copy, a "Sequence string" as required by 37 C.F.R. 1.821(c).
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.321(e).
content of the computer readacte form does not comply with the requirements of 37 O.F.R. (1320) and/or 1,323, as inclosed on the attached copy of the marked 40 fRaw Sequence Usage 1
and/or unreadable form that has been filed with this application has been found to be camaged computer readable as indicated on the attached CRF Diskette Problem Record. A Substitute computer readable form must be submitted as required by 37 0.F.R. (1305(d)).
5. The paper copy of the "Sequence Esting" is not the same as the computer readable from of the "Sequence Esting" as required by 37 C.F.R. (1321(e).
7. Other:
Applicant Must Provide:
An initial or substitute computer readable form (CRF) copy of the "Sequence Usting".
An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its
statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1,321(a) or 1,321(f) or 1,321(g) or
For questions regarding compliance to these requirements, please contact:

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For Rules Interpretation, call (703) 308-4216

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For Patentin software help, call (703) 308-6856

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, A--

1644

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000 TIME: 15:48:42

Input Set : A:\5647015.app

Output Set: N:\CRF3\05092000\H881509C.raw

ENTERED

```
5 (1) GENERAL INFORMATION:
 C-->
              (i) APPLICANT: SCHENDEL, Dolores J.
 C--> 9
              (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA
 C--> 11
             (iii) NUMBER OF SEQUENCES: 45
 C--> 13
             (iv) CORRESPONDENCE ADDRESS:
 C--> 14
                    (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
 C--> 15
                   (B) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
 C--> 16
                   (C) CITY: Washington
 C--> 17
                   (D) STATE: DC
 C--> 18
                   (E) COUNTRY: USA
 C--> 19
                   (F) ZIP: 20005-5701
 C--> 21
             (V) COMPUTER READABLE FORM:
 C--> 22
                   (A) MEDIUM TYPE: Floppy disk
 C--> 23
                   (B) COMPUTER: IBM PC compatible
                   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 C~-> 24
 C--> 25
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 C--> 27
             (vi) CURRENT APPLICATION DATA:
 C--> 28
                   (A) APPLICATION NUMBER: US/08/881,509C
 C--> 29
                   (B) FILING DATE: 24-Jun-1997
 C--> 30
                   (C) CLASSIFICATION:
C--> 32
           (Viii) ATTORNEY/AGENT INFORMATION:
C--> 33
                   (A) NAME: Kitts, Monica Chin
C--> 34
                   (B) REGISTRATION NUMBER: 36,105
C--> 35
                   (C) REFERENCE/DOCKET NUMBER: 564-7015
             (ix) TELECOMMUNICATION INFORMATION:
C--> 37
C--> 38
                   (A) TELEPHONE: (202) 638-5000
C--> 39
                   (B) TELEFAX: (202) 638-4810
    42 (2) INFORMATION FOR SEQ ID NO: 1:
C--> 44
             (i) SEQUENCE CHARACTERISTICS:
C--> 45
                  (A) LENGTH: 1341 base pairs
C--> 46
                   (B) TYPE: nucleic acid
C--> 47
                   (C) STRANDEDNESS: both
C--> 48
                   (D) TOPOLOGY: linear
C--> 50
            (ix) FEATURE:
C--> 51
                  (A) NAME/KEY: CDS
C--> 52
                  (B) LOCATION: 1..801
C--> 54
            (ix) FEATURE:
C--> 55
                  (A) NAME/KEY: sig_peptide
C--> 56
                  (B) LOCATION:1..54
C~-> 58
            (ix) FEATURE:
C--> 59
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C--> 60
                  (B) LOCATION: 55..801
C--> 62
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     65 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
66 -18 -15 -10 -5
                                                                                     48
     68 AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA
                                                                                     96
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000
TIME: 15:48:42

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Output Set: N:\CRF3\05092000\H881509C.raw

69 70	Ser	Leu	Ala 1	Lys	Thr	Thr	Gln 5	Pro	Ile	Ser	Met		Ser	Tyr	Glu	Gly		
		GAA			ΔΨΔ	ACC	ייים שריש	n.c.c	CAC	7.7.0		10	~~-			GAT		
73	Gln	Glu	Val	Agn	Tla	Thr	Cvc	RGC	CAC	AAC	AAC	ATT	GCT	ACA	AAT	GAT	14	4
74	15	014	, at	дэн	TIE	20	Cys	ser	HIS	Asn	Asn	He	Ala	Thr	Asn			
		ATC	ACC	TCC	ሞልሮ	C N N	CAC	mmm	000	100	25					30		
77	Tvr	Tle	Thr	TOO	Tur	Cln	CAG	Dha	000	AGC	CAA	GGA	CCA	CGA	TTT	ATT	19	2
78	- 2 -		1111	115	35	GIII	Gln	Pne	Pro	ser	GIn	GIY	Pro	Arg		Ile		
	ATT	CAA	GGA	ጥልሮ		DCD.	AAA	Cmm	3.03	40					45			
81	Tle	Gln	Glv	Tur	Tare	Thr	Lys	Val	ACA	AAC	GAA	GTG	GCC	TCC	CTG	TTT	24	0
82		·	013	50	шy з	1111	гÃ2	val	55	Asn	GIU	vaı	Ala		Leu	Phe		
84	ATC	ССТ	GCC		AGA	ΔAG	TCC	ACC.	3 C E	cmc	3.00	ama		60				
85	Ile	Pro	Ala	Asn	Arg	T.ve	Ser	Cor	Mp~	C T G	AGC	CTG	CCC	CGG	GTT	TCC	28	8
86			65	5	1119	Буз	261	70	1111	Leu	ser	Leu		Arg	Val	Ser		
88	CTG	AGC		АСТ	GCT	СТС	TAC	mac	mea	ama	CEC	a a m	75					
89	Leu	Ser	Asp	Thr	Ala	Val	Tyr	Tur	Cuc	tou	Uni	GGT	GGT	TCT	GCA	AGG	33	6
90		80				· u i	85	1 Y 1	Cys	Leu	Val	90	СТА	Ser	Ala	Arg		
92	CAA	CTG	ACC	ጥጥጥ	GGA	ጥርጥ	GGG	ACA	מאס	mmc	7 Cm	200	mm *					
93	Gln	Leu	Thr	Phe	Glv	Ser	Gly	Thr	C1n	LOU	mh~	Unl	TTA	CCT	GAT	ATC	38	4
94	95				1	100	OT,	1111	GIII	пец	105	Val	Leu	Pro	Asp			
96	CAG	AAC	CCT	GAC	CCT	GCC	GTG	ጥልሮ	CAC	CTC	707	CAC	mam		maa	110		
97	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	LAU	AUA	Acn	CON	AAA	TCC	AGT	432	2
98					115			-1-	OIII	120	nrg	vəħ	ser	ьуѕ		ser		
100	GAC	AAG	TCT	GTC		СТА	ידידי	ACC	' GAT	ւարդող	с д	тет	י מים ו	3.03	125	GTG		
101	Asp	Lys	Ser	Val	Cvs	Leu	Phe	Thr	Agn	Dhe) Aen	Cor	Cln	ALA . mb~	AAT	Val	4.8	30
102				130					135					140				
104	TCA	CAA	AGT	AAG	GAT	TCT	GAT	GTG	TAT	` ልጥሮ	ACA	GAC	י א א	140	CITIC	CTA		
105	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tvr	Tle	Thr	Aen	Luc	Thr	Val	Leu	52	38
TOO			145					150					155					
108	GAC	ATG	AGG	TCT	ATG	GAC	TTC	AAG	AGC	AAC	AGT	CCT	CTC	CCC	mcc	700		
109	Asp	Met	Arg	Ser	Met	Asp	Phe	Lvs	Ser	Asn	Ser	Ala	Val	Δla	Trn	AGC Cox	57	0
110		T00					165					170						
112	AAC	AAA	TCT	GAC	TTT	GCA	TGT	GCA	AAC	GCC	TTC	አአር	AAC	AGC	Δጥጥ	Δmm	62	
113	ASII	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Tla	Tla	02	4
T T 4	110					T80					185					100		
116	CCA	GAA	GAC	ACC	TTC	TTC	ccc	AGC	CCA	GAA	AGT	TCC	TGT	GAT	GTC	770	67	``
11/	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cvs	Asp	Val	Lvs	07	4
110					195					200					205			
120	CTG	GTC	GAG	AAA	AGC	TTT	GAA	ACA	GAT	ACG	AAC	CTA	AAC	TTT	CAA	AAC	72	Λ
121	Leu	Val	Glu	гÃг	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	12	٠
+42				210					215					220				
124	CTG	TCA	GTG	ATT	GGG	TTC	CGA	ATC	CTC	CTC	CTG	AAA	GTG	GCC	GGG	TTT	76	Ω
123	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Glv	Phe	, 0.	•
120			443					230					225					
128	AAT	CTG	CTC	ATG	ACG	CTG	CGG	CTG	TGG	TCC	AGC	TGAG	SATCI	GC A	AGAT	TGTA	A 821	1
127	Asn	пец	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser						02.	-
130	a	240					245											
132	GACA	GCCI	GT G	CTCC	CTCG	C TC	CTTC	CTCI	GCA	TTGC	CCC	TCTT	CTCC	CT C	TCCA	AACA	.G 881	1
134	AGGG	AACT	CT C	CTAC	CCCC	A AG	GAGG	TGAA	AGC	TGCT	'ACC	POOL	CTGT	GC C	CCCC	CGGC	A 941	
																	313	-

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Input Set : A:\5647015.app

Output Set: N:\CRF3\05092000\H881509C.raw

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136 ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA
138 CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA
                                                                                                 1001
                                                                                                 1061
      140 GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC
                                                                                                 1121
      142 CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCCTGGAG
                                                                                                 1181
      144 AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTCATA AAGAAATACA TAGTATTCTT
                                                                                                 1241
      146 CTTCTCAAGA CGTGGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG
                                                                                                 1301
      148 GGCGTGTTGT ATGTCCTGCT GCCGATGCCT TCATTAAAAT
                                                                                                1341
      151 (2) INFORMATION FOR SEQ ID NO: 2:
C--> 153
                (i) SEQUENCE CHARACTERISTICS:
C--> 154
                     (A) LENGTH: 267 amino acids
C--> 155
                     (B) TYPE: amino acid
C--> 156
                      (D) TOPOLOGY: linear
C--> 158
              (ii) MOLECULE TYPE: protein
C--> 160
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
     162 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu 163 -18 -15 -10 -5
     165 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly 166 1 10
     168 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp 169 15 20 25 30
     171 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
172 35 40 45
     174 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe 175 50 60
     177 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 178 65 70 75
     180 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
181 80 85 90
     183 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
184 95 100 105 110
     186 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 187 120 125
     189 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
190 130 135 140
     192 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
193 145 150 155
     195 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 166 165 170
    198 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
199 175 180 185 190
     201 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 202 205
    204 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn 205 210 215 220
    207 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
208 225 230 235
    210 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
211 240 245
    214 (2) INFORMATION FOR SEQ ID NO: 3:
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PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000 TIME: 15:48:42

Input Set : A:\5647015.app
Output Set: N:\CRF3\05092000\H881509C.raw

C>	216	;	(:	i) SI	EQUE:	NCE	CHAR	ACTE	RIST	cs:								
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C>	218	;						cleid			_							
C>	219)						NESS:										
C>	220	ı						lir										
C>			(i)	k) Fi			1001		icai									
C>			,				/KEV	. cnc	,									
C>								CDS										
C>							LION	19	133									
C>			(1 1	C) FE			/											
								sig		tide	•							
C>							LION:	16	3									
C>			(13	() FE														
C>								mat		tide	<u> </u>							
C>								64										
C>			(Xi	.) SE	QUEN	ICE I	ESCF	IPTI	ON:	SEQ	ID 1	10: 3	3:					
	236	ATG	GAT	' ACC	TGG	CTC	GTA	TGC	TGG	GCA	ATT	TTT	AGI	CTC	TTG	AAA	GCA	48
	231	Met	Asp	Thr	Trp	Leu	ı Val	Cys	Trp	Ala	Ile	Phe	Ser	Leu	Leu	Lys	Ala	
	238	- 21	- 20	1				-15					- 10)				
	240	GGA	CTC	ACA	GAA	CCI	GAA	GTC	ACC	CAG	ACT	CCC	AGC	CAT	CAG	GTC	ACA	96
	241	Gly	Leu	Thr	Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr	, ,
	242	- 5					1				- 5	i				10		
	244	CAG	ATG	GGA	CAG	GAA	GTG	ATC	TTG	CGC	TGT	GTC	CCC	ATC	TCT	AAT	CAC	144
	245	Gln	Met	Gly	Gln	Glu	Va1	Ile	Leu	Arg	Cys	Val	Pro	Ile	Ser	Asn	His	
	240				15					20					25			
	248	TTA	TAC	TTC	TAT	TGG	TAC	AGA	CAA	ATC	TTG	GGG	CAG	AAA	GTC	GAG	TTT	192
	249	Leu	Tyr	Pne	Tyr	Trp	Tyr	Arg	Gln	Ile	Leu	Gly	Gln	Lys	Val	Glu	Phe	
	250	ama	0.00	30					35					40				
	252	CTG	GTT	TCC	TTT	TAT	AAT	AAT	GAA	ATC	TCA	GAG	AAG	TCT	GAA	ATA	TTC	240
	254	neu	45	ser	Pne	Tyr	Asn	Asn	Glu	Ile	Ser	Glu			Glu	Ile	Phe	
		C A M			mmo			50					55					
	257	AGN	Van	CAA	TTC	TCA	GTT	GAA	AGG	CCT	GAT	GGA	TCA	AAT	TTC	ACT	CTG	288
	258	60	ASP	GIII	Pne	ser	val	Glu	Arg	Pro	Asp		Ser	Asn	Phe	Thr	Leu	
			N TO C	ccc	mea	101	65					70					75	
	261	Lare	Tlo	Ara	Com	Mb.	AAG	CTG	GAG	GAC	TCA	GCC	ATG	TAC	TTC	TGT	GCC	336
	262	шyэ	TIC	Arg	ser	80	гÃ2	Leu	GIU	Asp	Ser	Ala	Met	Tyr	Phe		Ala	
		ACC	ACC	CAA	» Cm		maa	mag	010	~~~	85					90		
	265	Ser	Sor	Clu	The	AAC	Com	TAC	GAG	CAG	TAC	TTC	GGG	CCG	GGC	ACC	AGG	384
	266	OC.	Det	GIU	95	MSII	ser	Tyr	GIU	GIN	Tyr	Phe	GIY	Pro		Thr	Arg	
		СТС	ACG	GTC		CAC	CAC	CTG	222	100	C.M.C.	mma			105			
	269	Len	Thr	Val	Thr	Clu	Acn	Leu	AAA	AAC	GTG	TTC	CCA	CCC	GAG	GTC	GCT	432
	270		1111	110	1111	GIU	Asp	пеп	115	ASII	Val	Pne	Pro		Glu	Val	Ala	
		GTG	ጥጥጥ		CCA	ጥሮአ	CAA	GCA	113	3 m.c	maa	a. a		120				
	273	Val	Phe	Glu	Pro	Ser	Glu	Ala	Clu	TIO	Com	CAC	ACC	CAA	AAG	GCC	ACA	480
	274		125	O L u	110	JCI	Giu	130	GIU	TTE	ser	HIS		GIn	Lys	Ala	Thr	
		CTG		TGC	СТС	GCC	ACA	GGC	ጥጥሮ	ሞአ <i>ር</i>	ccc	CAC	135	C T C	G 3 G	ama		
	277	Leu	Val	Cvs	Leu	Ala	Thr	Gly	Pho	Tur	Dro	Acr	UAC	GTG Wal	GAG	CTG	AGC	528
2	278	140		-,-	_~~	-1-4	145	O + 3	r 11C	+ X +	FIO		птр	۷al	GIU			
			TGG	GTG	ААТ	GGG	AAG	GAG	стс	CAC	ΔCT	150	cmc	100	202	C 2 C	155	
								-110	-10	CAC	2101	333	GIC	AGC	ACA	GAC	CCG	576

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PATENT APPLICATION: US/08/881,509C

Input Set : A:\5647015.app
Output Set: N:\CRF3\05092000\H881509C.raw

	281 282	Tr	Tr	Va]	l Ası	n Gly 160	/ Lys	s Glu	ı Val	His	Ser 165	Gly	Val	. Ser	Thr	Asp 170	Pro	
	284	CAC	CCC	CTC	CAAC	GAG	CAG	ccc	GCC	CTC	AAT	GAC	ጥሮር	' AGA	ጥልር	TOC	CTG	604
	283	GII	n Pro	Lei	Lys	Glu	ı Glr	Pro	Ala	Leu	Asn	Asp	Ser	Ara	Tvr	Cve	Leu	624
	286	1			1/5)				180					195			
	288	AGO	AGC	CGC	CTC	AGG	GTO	TCG	GCC	ACC	TTC	TGG	CAG	AAC	CCC	CCC	AAC	672
	289	Sei	: Ser	Arg	, Leτ	ı Arg	r Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Ara	Asn	072
	290			190)				195					200		_		
	292	CAC	TTC	CGC	TGT	CAA	GTC	CAG	TTC	TAC	GGG	CTC	TCG	GAG	AAT	GAC	GAG	720
	293	HIS	Phe	e Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	
	294		205)				210					215					
	290	TGG	ACC	CAG	GAT	AGG	GCC	AAA	CCT	GTC	ACC	CAG	ATC	GTC	AGC	GCC	GAG	768
	200	220	THE	GIN	Asp	Arg	Ala	Lys	Pro	Val	Thr		Ile	Val	Ser	Ala	Glu	
				CCT	מכת	CCZ	225		000			230					235	
	301	Δla	Trn	Clv	Aca	Ala	GAL	TGT	GGC	TTC	ACC	TCC	GAG	TCT	TAC	CAG	CAA	816
	302	· · · · ·	ııp	GIY	Arg	240	Asp	Cys	GIA	Pne	Thr	Ser	GLu	Ser	Tyr		Gln	
			GTC	CTG	ጥርጥ	GCC	A C C	ATC	CITIC	mam	245	3.000	mma		~~-	250		
	305	G1v	Val	Len	Ser	Δla	Thr	Ile	LOU	TAT	CAG	ATC	TIG	CTA	GGG	AAG	GCC	864
	306	2			255	1114	TILL	116	neu	260	GIU	116	ьeu	ьeu		rās	Ala	
	308	ACC	TTG	TAT			СТС	GTC	ልርጥ	CCC	CTC	CMC	CIDC	3 mc	265	3 ma	~~~	
	309	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Len	Val	LAU	Mo+	A I a	ATG	GTC	912
	310			270			~~~	• • •	275	ALU	neu	Val	ьeu	280	Ala	мет	val	
	312	AAG	AGA	AAG	GAT	TCC	AGA	GGC	TAG					200				026
	313	Lys	Arg	Lys	Asp	Ser	Arg	Gly										936
	314		285				_											
								290										
	317	(2)	INF	ORMA	rion	FOR	SEQ	ID N	10 : 4	! :								
C>	317 319	(2)	INF	ORMA	TION QUEN	FOR	SEQ HARA		10: 4 [STIC	l: CS:								
C>	317 319 320	(2)	INF) SE	QUEN	CE CI	IARA	ID N	STIC	cs:	ls							
C>	317 319 320 321	(2)	INF) SE((2 (1	QUENC A) LI B) T	CE CI ENGTI YPE:	HARAG H: 3 ami:	ID N CTERI ll an	ISTIC nino cid	cs:	ls							
C>	317 319 320 321 322	(2)	INFO) SE(() () (1	QUENCA) LI B) T' C) T(CE CI ENGTI YPE: OPOLO	HARAG H: 3 amin OGY:	ID N CTERI 11 am no ac line	ISTIC mino cid car	cs:	ls							
C> C>	317 319 320 321 322 324	(2)	INFO) SE(() () (1) () MO1	QUEN(A) L1 B) T; C) T(LECUI	CE CI ENGTI YPE: OPOLO LE TY	HARAG H: 3] amin)GY: (PE:	ID NOTERI	ISTIC mino cid car cein	S: acid								
C>	317 319 320 321 322 324 326		INFO (i (ii)) SE((1 (1 (1) MO1) SE(QUEN(A) L1 B) T C) T LECUI QUEN(CE CI ENGTI YPE: OPOLO LE TY CE DI	HARAGE: 3] amin DGY: (PE: ESCR)	ID NOTERI	ISTIC mino cid car cein	es: acid	D NO): 4 :						
C> C>	317 319 320 321 322 324 326 328	Met	(ii) (xi) Asp) SE((1 (1 (1) MO1) SE(QUEN(A) L1 B) T C) T LECUI QUEN(CE CI ENGTI YPE: OPOLO LE TY CE DI	HARAGE: 3] amin DGY: (PE: ESCR)	ID NOTERI	ISTIC mino cid car cein	es: acid	D NO	: 4: Phe	Ser	Leu	Leu	Lys	Ala	
C> C>	317 319 320 321 322 324 326 328 329	Met -21	(ii) (ii) (xi) Asp -20) SE((1 (1) (1) MO1) SE(Thr	QUENCA) LIB) TY CO) TC LECUI QUENC	CE CI ENGTI YPE: OPOLO LE TY CE DI Leu	HARAGE AMIR amir OGY: (PE: ESCR) Val	ID M CTERI 11 am no ac line prot PTIC Cys -15	STIC mino cid car cein ON: S	ES: acid EQ I Ala	D NO Ile	Phe	Ser					
C> C>	317 319 320 321 322 324 326 328 329 331	Met -21 Gly	(ii) (ii) (xi) Asp -20) SE((1 (1) (1) MO1) SE(Thr	QUENCA) LIB) TY CO) TC LECUI QUENC	CE CI ENGTI YPE: OPOLO LE TY CE DI Leu	HARAG H: 3] amin OGY: (PE: ESCR) Val Glu	ID M CTERI 11 am no ac line prot PTIC Cys -15	STIC mino cid car cein ON: S	ES: acid EQ I Ala	D NO Ile	Phe	Ser					
C> C>	317 319 320 321 322 324 326 328 329 331 332	Met -21 Gly -5	(ii) (xi) Asp -20 Leu	() (1) (1) (1) (1) (1) (1) (1) (1) (1) (QUENCA) LI B) TO C) TO LECUI QUENC Trp Glu	CE CI ENGTI YPE: DPOLO LE TY CE DE Leu	HARAGH: 31 amin OGY: VPE: ESCRI Val Glu 1	ID N CTERI 11 am no ac line prot PTIC Cys -15 Val	ISTICation aid ar cein ON: S Trp	CS: acid GEQ I Ala Gln	D NO Ile Thr 5	Phe Pro	Ser -10 Ser	His	Gln	Val	Thr	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334	Met -21 Gly -5	(ii) (xi) Asp -20 Leu	() (1) (1) (1) (1) (1) (1) (1) (1) (1) (QUENCA) LI B) TY C) TC LECUI QUENC Trp Glu Gln	CE CI ENGTI YPE: DPOLO LE TY CE DE Leu	HARAGH: 31 amin OGY: VPE: ESCRI Val Glu 1	ID M CTERI 11 am no ac line prot PTIC Cys -15	ISTIC mino eid ear cein ON: S Trp	ES: acid SEQ I Ala Gln Arg	D NO Ile Thr 5	Phe Pro Val	Ser -10 Ser	His	Gln	Val	Thr	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335	Met -21 Gly -5 Gln	(ii) (xi) Asp -20 Leu Met	() SE() () () MOI () SE() Thr	QUENCA) LI B) TY C) TC LECUI QUENC Trp Glu Gln 15	CE CIENGTI YPE: OPOLO LE TY LE DI Leu Pro Glu	HARAGH: 31 amin DGY: (PE: ESCRI Val Glu 1 Val	ID N CTERI 11 am no ac line prot Cys -15 Val	ISTIC mino cid ear cein ON: S Trp Thr	ES: acid SEQ I Ala Gln Arg	D NO Ile Thr 5 Cys	Phe Pro Val	Ser -10 Ser Pro	His Ile	Gln Ser	Val 10 Asn	Thr His	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337	Met -21 Gly -5 Gln	(ii) (xi) Asp -20 Leu Met	() SE(() () () MOI) SE(() Thr Thr Gly Phe	QUENCA) LI B) TY C) TC LECUI QUENC Trp Glu Gln 15	CE CIENGTI YPE: OPOLO LE TY LE DI Leu Pro Glu	HARAGH: 31 amin DGY: (PE: ESCRI Val Glu 1 Val	ID N CTERI 11 am no ac line prot PTIC Cys -15 Val	ISTICATION OF THE COLUMN TO THE COLUMN THE C	ES: acid SEQ I Ala Gln Arg	D NO Ile Thr 5 Cys	Phe Pro Val	Ser -10 Ser Pro	His Ile	Gln Ser	Val 10 Asn	Thr His	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337 338	Met -21 Gly -5 Gln Leu	(ii) (xi) Asp -20 Leu Met	() SE(() () MOI) SE(() Thr Thr Gly Phe 30	QUENCA) LI B) TO CO CO TO CO T	CE CIENGTI YPE: OPOLO LE TY LE DI Leu Pro Glu Trp	HARAGE AMIN OGY: (PE: ESCRI Val Glu 1 Val Tyr	ID N CTERI II am no ac line prot PTIC Cys -15 Val Ile Arg	ISTIC mino cid ear cein ON: S Trp Thr Leu Gln 35	ES: acid SEQ I Ala Gln Arg 20 Ile	D NO Ile Thr 5 Cys	Phe Pro Val Gly	Ser -10 Ser Pro	His Ile Lys	Gln Ser 25 Val	Val 10 Asn Glu	Thr His Phe	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337 338 340	Met -21 Gly -5 Gln Leu	(ii) (ii) (xi) Asp -20 Leu Met Tyr	() SE(() () () MOI) SE(() Thr Thr Gly Phe 30	QUENCA) LI B) TO CO CO TO CO T	CE CIENGTI YPE: OPOLO LE TY LE DI Leu Pro Glu Trp	HARAGE AMIN OGY: (PE: ESCRI Val Glu 1 Val Tyr	ID NOTERIAL INCOME. ID ATTEMPTS TO A TO	ISTIC mino cid ear cein ON: S Trp Thr Leu Gln 35	ES: acid SEQ I Ala Gln Arg 20 Ile	D NO Ile Thr 5 Cys	Phe Pro Val Gly	Ser -10 Ser Pro Gln Lys	His Ile Lys	Gln Ser 25 Val	Val 10 Asn Glu	Thr His Phe	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337 338 340 341	Met -21 Gly -5 Gln Leu Leu	(ii) (xi) (xi) Asp -20 Leu Met Tyr Val 45	() SE() (1) (1) MOI) SE() Thr Thr Gly Phe 30 Ser	QUENCA) LI B) TY C) TC CUENC Trp Glu Gln 15 Tyr Phe	CE CIENGTI VPE: DPOLO LE TY LE DI Leu Pro Glu Trp Tyr	HARACH: 3: amin DGY: CPE: ESCRI Val Glu 1 Val Tyr Asn	ID NOTERIAL INCOME. IN THE PROPERTY OF THE PRO	ESTICATION OF THE COLUMN TO THE COLUMN THE C	ES: acid EEQ I Ala Gln Arg 20 Ile	D NO Ile Thr 5 Cys Leu (Phe Pro Val Gly	Ser -10 Ser Pro Gln Lys	His Ile Lys 40 Ser	Gln Ser 25 Val Glu	Val 10 Asn Glu Ile	Thr His Phe Phe	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337 338 340 341	Met -21 Gly -5 Gln Leu Leu	(ii) (xi) (xi) Asp -20 Leu Met Tyr Val 45	() SE() (1) (1) MOI) SE() Thr Thr Gly Phe 30 Ser	QUENCA) LI B) TY C) TC CUENC Trp Glu Gln 15 Tyr Phe	CE CIENGTI VPE: DPOLO LE TY LE DI Leu Pro Glu Trp Tyr	HARAGE AMIN OGY: OGY: OFE: SCRI Val Glu 1 Val Tyr Asn	ID NOTERIAL INCOME. ID ATTEMPTS TO A TO	ESTICATION OF THE COLUMN TO THE COLUMN THE C	ES: acid EEQ I Ala Gln Arg 20 Ile	D NO Ile Thr 5 Cys Leu (Phe Pro Val Gly Glu	Ser -10 Ser Pro Gln Lys	His Ile Lys 40 Ser	Gln Ser 25 Val Glu	Val 10 Asn Glu Ile	Thr His Phe Phe Leu	
C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337 338 340 341 343	Met -21 Gly -5 Gln Leu Leu Asp 60	(ii) (xi) Asp -20 Leu Met Tyr Val 45 Asp	() SE((1) MOI () SE(Thr Thr Gly Phe 30 Ser	QUENCA) LIBS) TYPO Glu Gln 15 Tyr Phe Phe	CE CIENGTHE YPE: DPOLO LE TY LE DE Leu Pro Glu Trp Tyr Ser	HARACH: 3: amin OGY: CPE: ESCRI Val Glu 1 Val Tyr Asn Val 65	ID NOTERIAL INCOME. ID NOTERIAL INCOME. ID NOTERIAL IDEA Arg Asn 500 Glu	mino cid car cein ON: S Trp Thr Leu Gln 35 Glu Arg	ES: acid	D NO Ile Thr 5 Cys Leu Ser (Phe Pro Val Gly Glu	Ser -10 Ser Pro Gln Lys 55 Ser	His Ile Lys 40 Ser	Gln Ser 25 Val Glu	Val 10 Asn Glu Ile	Thr His Phe Phe Leu	
C> C> C>	317 319 320 321 322 324 326 328 329 331 332 334 335 337 338 340 341 343	Met -21 Gly -5 Gln Leu Leu Asp 60	(ii) (xi) Asp -20 Leu Met Tyr Val 45 Asp	() SE() (1) MOI) SE() Thr Thr Gly Phe 30 Ser Gln	QUENCA) LIBS) TYPO Glu Gln 15 Tyr Phe Phe	CE CIENGTI YPE: DPOLO LE TY LE DI Leu Pro Glu Trp Tyr Ser Thr	HARACH: 3: amin OGY: CPE: ESCRI Val Glu 1 Val Tyr Asn Val 65	ID NOTERIAL INCOME. IN THE PROPERTY OF THE PRO	mino cid car cein ON: S Trp Thr Leu Gln 35 Glu Arg	ES: acid	D NO Ile Thr 5 Cys Leu Ser Asp	Phe Pro Val Gly Glu	Ser -10 Ser Pro Gln Lys 55 Ser	His Ile Lys 40 Ser	Gln Ser 25 Val Glu	Val 10 Asn Glu Ile Thr	Thr His Phe Phe Leu	
C> C> C>	317 319 320 321 322 324 326 328 331 331 335 337 338 340 341 343 344 346 347	Met -21 Gly -5 Gln Leu Leu Asp 60 Lys	INFF (ii (iii) (xii) Asp -20 Leu Met Tyr Val 45 Asp	(i) (ii) MOI) SE(iii) MOI) SE(iiii) Thr Thr Gly Phe 30 Ser Gln Arg	QUENCAA) LI ABB) T: CONTROL TO CONTROL	CE CIENGTHE YPE: DPOLO LE TY LEU Pro Glu Trp Tyr Ser Thr 80	HARACH: 31 amin DGY: CPE: ESCRI Val Glu 1 Val Tyr Asn Val 65 Lys	ID N CTERN 11 am no ac line prot Cys -15 Val Ile Arg Asn 50 Glu Leu	ear sein on seid sear sein on: S Trp Thr Leu Gln 35 Glu Arg	ES: acid SEQ I Ala Gln Arg 20 Ile: Ile:	D NO Ile Thr 5 Cys Leu Ser Asp	Phe Pro Val Gly Glu Gly 70 Ala	Ser -10 Ser Pro Gln Lys 55 Ser	His Ile Lys 40 Ser Asn	Gln Ser 25 Val Glu Phe	Val 10 Asn Glu Ile Thr	Thr His Phe Phe Leu 75 Ala	
C> C> C>	317 319 320 321 322 324 326 328 331 331 335 337 338 340 341 343 344 346 347	Met -21 Gly -5 Gln Leu Leu Asp 60 Lys	INFF (ii (iii) (xii) Asp -20 Leu Met Tyr Val 45 Asp	(i) (ii) MOI) SE(iii) MOI) SE(iiii) Thr Thr Gly Phe 30 Ser Gln Arg	QUENCAA) LI ABB) T: CONTROL TO CONTROL	CE CIENGTHE YPE: DPOLO LE TY LEU Pro Glu Trp Tyr Ser Thr 80	HARACH: 31 amin DGY: CPE: ESCRI Val Glu 1 Val Tyr Asn Val 65 Lys	ID NOTERIAL INCOME. ID NOTERIAL INCOME. ID NOTERIAL IDEA Arg Asn 500 Glu	estionino cid car cein N: S Trp Thr Leu Gln 35 Glu Arg Glu	ES: acid SEQ I Ala Gln Arg 20 Ile: Ile:	D NO Ile Thr 5 Cys Leu Ser Asp	Phe Pro Val Gly Glu Gly 70 Ala	Ser -10 Ser Pro Gln Lys 55 Ser	His Ile Lys 40 Ser Asn Tyr	Gln Ser 25 Val Glu Phe	Val 10 Asn Glu Ile Thr	Thr His Phe Phe Leu 75 Ala	

VERIFICATION SUMMARY DATE: 05/09/2000 PATENT APPLICATION: US/08/881,509C TIME: 15:48:43 Input Set : A:\5647015.app Output Set: N:\CRF3\05092000\H881509C.raw L:7 M:220 C: Keyword misspelled, [(i) APPLICANT:] L:9 M:220 C: Keyword misspelled, [(ii) TITLE OF INVENTION:] L:11 M:220 C: Keyword misspelled, [(iii) NUMBER OF SEQUENCES:] L:13 M:220 C: Keyword misspelled, [(iv) CORRESPONDENCE ADDRESS:] L:14 M:220 C: Keyword misspelled, [(A) ADDRESSEE:] L:15 M:220 C: Keyword misspelled, [(B) STREET:] L:16 M:220 C: Keyword misspelled, [(C) CITY:] L:17 M:220 C: Keyword misspelled, [(D) STATE:] L:18 M:220 C: Keyword misspelled, [(E) COUNTRY:] L:19 M:220 C: Keyword misspelled, [(F) ZIP:] L:21 M:220 C: Keyword misspelled, [(v) COMPUTER READABLE FORM:] L:22 M:220 C: Keyword misspelled, [(A) MEDIUM TYPE:] L:23 M:220 C: Keyword misspelled, [(B) COMPUTER:]
L:24 M:220 C: Keyword misspelled, [(C) OPERATING SYSTEM:] L:25 M:220 C: Keyword misspelled, [(D) SOFTWARE:] L:27 M:220 C: Keyword misspelled, [(vi) CURRENT APPLICATION DATA:] L:28 M:220 C: Keyword misspelled, [(A) APPLICATION NUMBER:] L:29 M:220 C: Keyword misspelled, [(B) FILING DATE:] L:30 M:220 C: Keyword misspelled, [(C) CLASSIFICATION:] L:32 M:220 C: Keyword misspelled, [(viii) ATTORNEY/AGENT INFORMATION:] L:33 M:220 C: Keyword misspelled, [(A) NAME:] L:34 M:220 C: Keyword misspelled, [(B) REGISTRATION NUMBER:] L:35 M:220 C: Keyword misspelled, [(C) REFERENCE/DOCKET NUMBER:] L:37 M:220 C: Keyword misspelled, [(ix) TELECOMMUNICATION INFORMATION:] L:38 M:220 C: Keyword misspelled, [(A) TELEPHONE:] L:39 M:220 C: Keyword misspelled, [(B) TELEFAX:] L:44 M:220 C: Keyword misspelled, [(i) SEQUENCE CHARACTERISTICS:] L:45 M:220 C: Keyword misspelled, [(A) LENGTH:] L:46 M:220 C: Keyword misspelled, [(B) TYPE:] L:47 M:220 C: Keyword misspelled, [(C) STRANDEDNESS:] L:48 M:220 C: Keyword misspelled, [(D) TOPOLOGY:] L:50 M:220 C: Keyword misspelled, [(ix) FEATURE:] L:51 M:220 C: Keyword misspelled, [(A) NAME/KEY:] L:52 M:220 C: Keyword misspelled, [(B) LOCATION:] L:54 M:220 C: Keyword misspelled, [(ix) FEATURE:] L:55 M:220 C: Keyword misspelled, [(A) NAME/KEY:] L:56 M:220 C: Keyword misspelled, [(B) LOCATION:] L:58 M:220 C: Keyword misspelled, [(ix) FEATURE:] L:59 M:220 C: Keyword misspelled, [(A) NAME/KEY:] L:60 M:220 C: Keyword misspelled, [(B) LOCATION:]
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VERIFICATION SUMMARY
PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000
TIME: 15:48:43

Input Set : A:\5647015.app

Output Set: N:\CRF3\05092000\H881509C.raw

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 L:218 M:220 C: Keyword misspelled, [(B) TYPE:]
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 L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:507 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
 L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:609 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:643 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23, Value=[not relevant]
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
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L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:737 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25, Value=[not relevant] L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
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L:1068 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=45, Value=[not relevant]
L{:}1080~M{:}341~W{:} (46) "n" or "Xaa" used, for SEQ ID#:45
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